## **Artemis ACT**

ACT (Artemis Comparison Tool) is a viewer based on Artemis that allows examining pair-wise genome DNA sequence comparisons. IMG only creates data files that are compatible with Artemis ACT. Moreover, metagenomes are supported by this tool.

In order to run Artemis ACT, users are required to have the following:

- Java: <a href="http://www.java.com/en/">http://www.java.com/en/</a>
- Artmeis ACT: <a href="http://www.sanger.ac.uk/science/tools/artemis-comparison-tool-act">http://www.sanger.ac.uk/science/tools/artemis-comparison-tool-act</a>

The first step of using ACT involves selecting from 2 to 5 genomes of interest, as illustrated in Figure 1(i), where *Ralstonia eutropha JMP134* and *Ralstonia insidiosa ATCC 49129* are selected from the list of finished bacterial genomes. Two filters (Sequencing Status, Domain) can be used to select the list of all isolate genomes available in IMG.

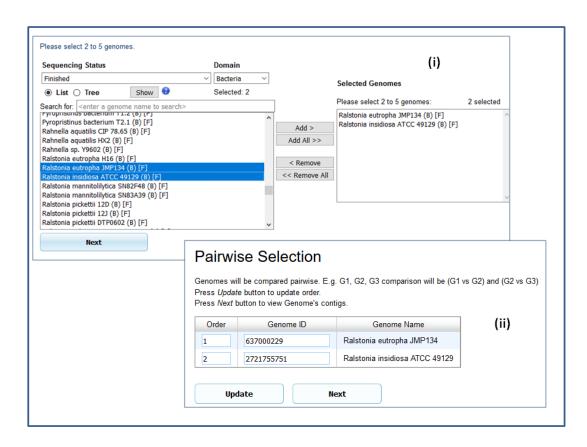


Figure 1. Artemis ACT: Genome Selection and Pairwise Selection.

The selected genomes are compared in pairs, where the pairs are determined by the order in which the genomes were selected. For example, if genomes G1, G2, G3, and G4 were selected, the G1 will be compared to G2, G2 will be compared to G3, and G3 will be compared to G4. The pairwise comparisons can be adjusted using the Pairwise Selection page, as shown in Figure 1(ii). Users can reorder the selected genomes by changing the values in the "Order" column and click the "Update" button.

After the user clicks the "Next" button, all the scaffolds and contigs of the selected genomes are displayed in the Contig Reorder page, as illustrated in Figure 2(i). This page can be used to remove the contigs that should not be included in the comparison, as well as for reordering the contigs that are included. To remove any contigs in the analysis, simply check the corresponding "Ignore" column. Updating values in the "Order" column allows selected contigs to be reordered. Click the "Update" button to confirm the removal and/or reordering, and click the "Next" button to continue.

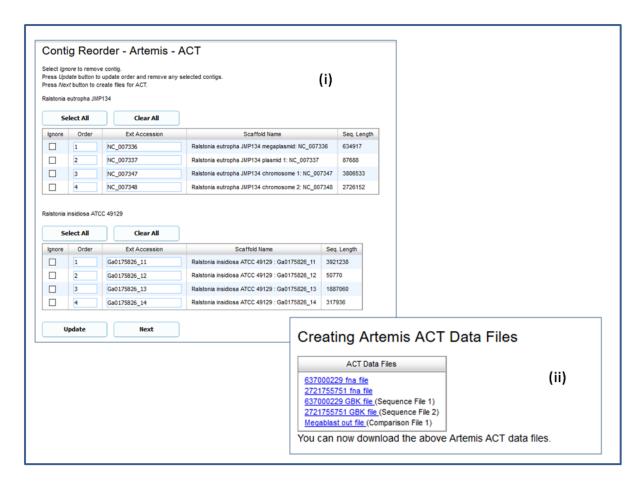


Figure 2. Artemis ACT: Contig Reordering and Creating Data Files.

Three types of output files will be generated for downloading (See Figure 2(ii):

- DNA sequence fna files.
- Genbank GBK files.
- Metablast comparison output file.

**Reference:** Carver, T.J., Rutherford, K.M., Berriman, M. et al. (2005) ACT: the Artemis Comparison Tool. Bioinformatics 21(16): 3422-3423.